141287

STIC-Biotech/ChemLib

From:	Romeo, David
Sent:	Monday, December 27, 2004 6:24 PM
To:	STIC-Biotech/ChemLib
Subject:	10014162

```
'Requester's Name: ... David Romeo
    Serial Number: ... 10014162
         Art Unit: ... 1647
           Office: ... REM 4D39
          Mailbox: ... REM 4C70
            Phone: ... 571 272-0890
 Date of Request: ... 12/27/2004
*******************************************************
```

PLEASE PROVIDE RESULTS ON DISK(s)

Search the commercial/public and interference files for SEQ ID NO: 1.

****
Type of Search
NA Sequence: #_____
AA Sequence :#____/_____
Structure: #_____
Bibliographic:_____
Litigation:_____
Patent Family:_____
Other:_____

GenCore version 5.1.6
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Run on: December 29, 2004, 15:22:36 ; Search time 156 Seconds
(without alignments)
89.682 Million cell updates/sec

Titles:
Sequence: 1 SLALADDAPRERARLLAALERHRHLMSYMHKILIVLDAP 39
Perfect score: 196
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Maximum DB seq length: 2000000000
Minimum DB seq length: 0

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: geneseq_23Sep04.*
A. Geneseq_23Sep04:*
1: geneseqp1980da:*
2: geneseqp2000ds:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2002s:*
7: geneseqp2003sa:*
8: geneseqp2004s:*

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	196	100.0	39	4	Aab80490	AAB80490	PTH2 rece
2	196	100.0	39	4	Aae23970	AAE23970	Human TIP
3	196	100.0	39	4	Aab82202	AAB82202	TIP39 pol
4	196	100.0	39	4	Abp56764	ABP56764	Human TIP
5	196	100.0	40	5	Aau73101	AAU73101	Parathyro
6	196	100.0	39	4	Aae23969	AAE23969	Human TIP
7	196	100.0	100	5	Aab82210	AAB82210	Human TIP
8	196	100.0	100	5	Abp56763	ABP56763	Human TIP
9	196	100.0	38	4	Aab80489	AAB80489	PTH2 rece
10	189	96.4	38	4	Aab80526	AAB80526	PTH2 rece
11	189	95.9	37	4	Aab80408	AAB80408	PTH2 rece
12	188	95.9	37	4	Aab82197	AAB82197	TIP39 tru
13	185	94.4	37	4	Aab80525	AAB80525	PTH2 rece
14	184	93.9	36	4	Aab80487	AAB80487	PTH2 rece
15	180	91.8	35	4	Aab80527	AAB80527	PTH2 rece
16	180	91.8	35	4	Aab80486	AAB80486	PTH2 rece
17	179	91.3	35	4	Aab80524	AAB80524	PTH2 rece
18	176	89.8	34	4	Aab80528	AAB80528	PTH2 rece
19	176	89.8	34	4	Aab80485	AAB80485	PTH2 rece
20	175	89.3	35	4	Aab80523	AAB80523	PTH2 rece
21	172	87.8	100	5	Abb82211	Mouse TIP

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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Run on: December 29, 2004, 15:03:39 ; Search time 37 Seconds
(without alignments)
69.903 Million cell updates/sec

Titles:
Sequence: 1 SLALADDAPRERARLLAALERHRHLMSYMHKILIVLDAP 39
Perfect score: 196
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Maximum DB seq length: 2000000000
Minimum DB seq length: 0

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptcdata/1/iss/5A_COMB.pep:*
2: /cgn2_6/ptcdata/1/iss/5B_COMB.pep:*
3: /cgn2_6/ptcdata/1/iss/6A_COMB.pep:*
4: /cgn2_6/ptcdata/1/iss/6B_COMB.pep:*
5: /cgn2_6/ptcdata/1/iss/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/1/iss/backfile1.pep:*
Issued_patents_AA:*

Result No.	Score	% Query Match	Length	DB	ID	Description
22	172	87.8	100	6	Abp56765	Mouse TIP
23	171	87.2	34	4	Abp56752	PTH2 rece
24	170	86.7	33	4	Aab80484	PTH2 rece
25	170	86.7	33	4	Aab80529	PTH2 rece
26	167	85.7	32	4	Aab80521	PTH2 rece
27	164	83.7	31	4	Aab80483	PTH2 rece
28	164	83.7	32	4	Aab82199	TIP39 tru
29	164	83.7	32	4	Abb82198	TIP39 tru
30	161	82.1	32	4	Aab80520	PTH2 rece
31	161	82.1	31	4	Aab80531	PTH2 rece
32	160	81.6	31	4	Aab80482	PTH2 rece
33	160	81.6	31	4	Aab80530	PTH2 rece
34	158	80.6	30	4	Aab80519	TIP39 tru
35	158	80.6	30	4	Aab80481	PTH2 rece
36	156	79.6	30	4	Aab80532	PTH2 rece
37	156	79.6	30	4	Aab82199	TIP39 tru
38	156	79.6	30	4	Aab80480	PTH2 rece
39	150	76.5	29	4	Aab80518	TIP39 tru
40	150	76.5	29	4	Aab80533	PTH2 rece
41	150	76.5	29	4	Aab82208	PTH2 rece
42	150	76.5	29	4	Aab82200	Chimeric
43	145	74.0	28	4	Aab80479	PTH2 rece
44	145	74.0	28	4	Aab82208	PTH2 rece
45	145	74.0	28	4	Abb82201	TIP39 tru

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Title: OM protein - protein search, using sw model
Perfect score: 196
Sequence: 1 SLALADDAAFREBARLLAALERRHWLNSYMHKLLVLDAR 39

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Run on: December 29, 2004, 15:12:10 / Search time 144 Seconds
                (without alignments)
                97.426 Million cell updates/sec

ALIGNMENTS   GenCore version 1.6
                Copyright (c) 1993 - 2004 Compugen Ltd.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	196	100.0	196		US-09-843-221A-160	Sequence 160, App
2	58	26.5	39	4	US-09-843-221A-170	Sequence 170, App
3	58	29.1	651		US-09-252-991A-18065	Sequence 18065, A
4	57	29.1	216		US-09-252-991A-26519	Sequence 26519, A
5	55.5	28.3	736		US-09-731-981-2	Sequence 2, Appl
6	55.5	28.1	736		US-09-600-971-2	Sequence 2, Appl
7	55	28.3	736		US-10-096-961A-2	Sequence 2, Appl
8	55	27.0	6095		US-10-085-2	Sequence 2, Appl
9	53	28.1	248		US-09-248-796A-15408	Sequence 15408, A
10	52	26.5	252		US-09-489-931A-28324	Sequence 28324, A
11	52	26.5	679		US-09-489-931A-28325	Sequence 28325, A
12	51	26.5	723		US-09-434-408-2	Sequence 2, Appli
13	51	26.0	304		US-09-543-681A-4631	Sequence 4631, A
14	51	25.8	221		US-09-489-039A-10862	Sequence 10862, A
15	50.5	25.5	198		US-09-248-796A-1642	Sequence 1642, A
16	50	25.5	254		US-09-248-796A-1621	Sequence 1621, A
17	50	25.5	315		US-09-134-000C-6449	Sequence 6449, A
18	50	25.8	323		US-09-489-039A-12496	Sequence 12496, A
19	50	25.5	583		US-09-252-991A-32735	Sequence 32735, A
20	50	25.5	563		US-08-311-731A-142	Sequence 142, Appl
21	49.5	25.3	850		US-09-904-389-2	Sequence 2, Appli
22	49.5	25.3	563		US-08-311-731A-142	Sequence 142, Appl
23	49	25.0	48		5182364-1	Patent No. 5182364
24	49	25.0	48		5168045-6	Patent No. 5168045
25	49	25.0	172		US-09-489-039A-8648	Sequence 8648, A
26	49	25.0	372		US-10-265-012-14	Sequence 14, Appl
27	49	25.0	434		US-10-265-012-10	Sequence 10, Appl
28	49	25.0	507		US-09-489-039A-10267	Sequence 10267, A
29	49	25.0	569		US-10-265-012-12	Sequence 12, Appl
30	49	25.0	156		US-10-265-012-8	Sequence 8, Appl
31	49	25.0	280		US-09-489-039A-10266	Sequence 10266, A
32	49	25.0	875		US-09-489-931A-15400	Sequence 15400, A
33	49	25.0	679		US-09-489-931A-25400	Sequence 25400, A
34	48.5	25.0	156		US-09-540-236-2047	Sequence 2047, A
35	48.5	24.7	478		US-09-489-931A-30056	Sequence 30056, A
36	48	24.7	599		US-09-252-991A-12663	Sequence 12663, A
37	48	24.5	1099		US-09-876-548	Sequence 5948, Ap
38	48	24.5	320		US-09-489-039A-10093	Sequence 10093, A
39	48	24.5	369		US-09-489-039A-12248	Sequence 12248, A
40	48	24.5	369		US-09-489-039A-12768	Sequence 12768, A
41	47.5	24.2	320		US-10-399-037-1706	Sequence 1706, A
42	47.5	24.2	110		US-09-489-039A-24411	Sequence 24411, A
43	47.5	24.0	110		US-09-252-991A-30676	Sequence 30676, A
44	47	24.0	110		US-10-270-767-24959	Sequence 24959, A
45	47	24.0	158		US-09-489-039A-19915	Sequence 47313, A
45	47	24.0	158		US-10-252-991A-20822	Sequence 20822, A

Searched: 1599051 aego, 359727711 residues   1599051

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications Aa.*
1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep:*
4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
6: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep:*
7: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep:*
8: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep:*
9: /cgn2_6/prodata/2/pubpaa/US09B_PUBCOMB.pep:*
10: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep:*
11: /cgn2_6/prodata/2/pubpaa/US09D_PUBCOMB.pep:*
12: /cgn2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep:*
13: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep:*
14: /cgn2_6/prodata/2/pubpaa/US10C_NEW_PUB.pep:*
15: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep:*
16: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep:*
19: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep:*
20: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	196	100.0	10		US-09-843-221A-160	Sequence 160, App
2	196	100.0	39	4	US-09-843-221A-170	Sequence 170, App
3	196	100.0	196		US-10-014-162-1	Sequence 1, Appli
4	196	100.0	38		US-09-843-221A-170	Sequence 170, App
5	196	100.0	16		US-10-399-602-12	Sequence 12, Appl
6	196	100.0	39		US-10-466-493A-2	Sequence 2, App
7	196	100.0	39		US-10-014-162-39	Sequence 39, Appl
8	196	100.0	39		US-10-466-493A-2	Sequence 2, Appl
9	196	100.0	17		US-10-014-162-6	Sequence 6, Appl
10	196	100.0	39		US-10-466-493A-41	Sequence 41, Appl
11	98.0	98.0	100		US-10-839-037-1706	Sequence 11, Appl
12	98.0	98.0	14		US-10-399-602-13	Sequence 13, Appl
13	95.9	95.9	38		US-10-466-493A-31	Sequence 2, Appli
14	95.9	95.9	37		US-10-014-162-38	Sequence 160, App
15	94.4	94.4	36		US-10-014-162-2	Sequence 2, Appl
16	93.3	93.3	36		US-10-466-493A-2	Sequence 32, Appl
17	91.3	91.3	34		US-10-014-162-40	Sequence 42, Appl
18	89.8	89.8	34		US-10-399-602-11	Sequence 6, Appl
19	89.3	89.3	179		US-10-014-162-6	Sequence 170, App
20	87.8	87.8	14		US-10-399-602-3	Sequence 3, Appl
21	87.8	87.8	16		US-10-466-493A-14	Sequence 11, Appl
22	87.8	87.8	100		US-10-839-037-1706	Sequence 13, Appl
23	87.8	87.8	16		US-10-466-493A-32	Sequence 32, Appl
24	87.3	87.3	16		US-10-466-493A-32	Sequence 32, Appl
25	87.3	87.3	34		US-10-014-162-42	Sequence 42, Appl

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 29, 2004, 15:02:54. Search time 468 seconds

ALIGNMENTS

Title: US-10-014-162-1
Perfect score: 196
Sequence: 1 SLALADDAAFRERARLLAALERRHWLNSTMHKKLLVLDAP 39

Scoring table: BLOSUM62
Searched: Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters:
6730630 seqs, 1107996698 residues   6730630

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Databases :
Pending Patents_AA_Main:*
1: /cgn2_6/ptcdata/1/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptcdata/1/paa/US06_COMB.pep:*
3: /cgn2_6/ptcdata/1/paa/US07_COMB.pep:*
4: /cgn2_6/ptcdata/1/paa/US080_COMB.pep:*
5: /cgn2_6/ptcdata/1/paa/US081_COMB.pep:*
6: /cgn2_6/ptcdata/1/paa/US082_COMB.pep:*
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8: /cgn2_6/ptcdata/1/paa/US085_COMB.pep:*
9: /cgn2_6/ptcdata/1/paa/US087_COMB.pep:*
10: /cgn2_6/ptcdata/1/paa/US089_COMB.pep:*
11: /cgn2_6/ptcdata/1/paa/US090_COMB.pep:*
12: /cgn2_6/ptcdata/1/paa/US092_COMB.pep:*
13: /cgn2_6/ptcdata/1/paa/US093_COMB.pep:*
14: /cgn2_6/ptcdata/1/paa/US105_COMB.pep:*
15: /cgn2_6/ptcdata/1/paa/US091_COMB.pep:*
16: /cgn2_6/ptcdata/1/paa/US092_COMB.pep:*

	Score	%			
26	170	86.7	33	14	US-10-014-162-7 Sequence 7, Appli
27	170	86.7	33	17	US-10-428-377-23 Sequence 23, Appli
28	170	86.7	33	17	US-10-428-377-27 Sequence 27, Appli
29	167	85.2	33	14	US-10-014-162-43 Sequence 43, Appli
30	167	85.2	33	14	US-10-014-162-23 Sequence 23, Appli
31	164	83.7	33	14	US-10-014-162-3 Sequence 3, Appli
32	164	83.7	33	17	US-10-428-377-26 Sequence 26, Appli
33	163	83.2	33	14	US-10-014-162-44 Sequence 44, Appli
34	160	81.6	31	14	US-10-014-162-9 Sequence 9, Appli
35	160	81.6	31	14	US-10-014-162-78 Sequence 70, Appli
36	160	81.6	31	14	US-10-466-493A-51 Sequence 51, Appli
37	156	79.6	30	14	US-10-014-162-45 Sequence 45, Appli
38	156	79.6	30	14	US-10-014-162-10 Sequence 10, Appli
39	156	79.6	30	14	US-10-014-162-79 Sequence 1, Appli
40	156	79.6	30	14	US-10-466-493A-44 Sequence 44, Appli
41	156	79.6	30	14	US-10-466-493A-1 Sequence 1, Appli
42	156	79.6	29	16	US-10-014-162-80 Sequence 80, Appli
43	150	76.5	29	16	US-10-466-493A-5 Sequence 5, Appli
44	150	76.5		16	US-10-014-162-46 Sequence 46, Appli
45	150	76.5	37	16	US-10-466-493A-13 Sequence 13, Appli

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	196	100.0	39	PCT-US01-11954-12	Sequence 12, Appli
2	196	100.0	39	PCT-US01-11954-14	Sequence 14, Appli
3	196	100.0	39	PCT-US02-01183-7	Sequence 3, Appli
4	196	100.0	39	PCT-US02-18771-3	Sequence 3, Appli
5	196	100.0	39	US-10-399-602-32	Sequence 32, Appli
6	196	100.0	39	US-10-014-162-1	Sequence 1, Appli
7	196	100.0	39	US-10-466-493A-7	Sequence 7, Appli
8	196	100.0	39	US-10-599A-14	Sequence 14, App
9	196	100.0	34	US-10-839-037-160	Sequence 160, App
10	196	100.0	36	US-10-839-037-170	Sequence 170, App
11	196	100.0	37	US-10-839-037-1	Sequence 1, Appli
12	192	97.9	37	PCT-US02-18771-2	Sequence 2, Appli
13	188	95.9	29	PCT-US02-01183-31	Sequence 31, Appli
14	188	95.9	29	PCT-US02-01183-31	Sequence 31, Appli
15	188	95.9	36	US-10-399-602-2	Sequence 2, Appli
16	188	95.9	36	US-10-466-493A-2	Sequence 2, Appli
17	188	95.9	37	US-10-466-493A-31	Sequence 31, Appli
18	185	93.9	36	US-10-014-162-60	Sequence 60, Appli
19	184	93.9	36	US-10-014-162-4	Sequence 4, Appli
20	180	91.8	36	US-10-014-162-5	Sequence 5, Appli
21	179	91.3	36	US-10-014-162-61	Sequence 61, Appli
22	176	89.3	36	US-10-014-162-6	Sequence 6, Appli
23	175	89.3	39	US-10-014-162-8	Sequence 8, Appli
24	172	87.8	39	US-10-839A-11	Sequence 11, Appli
25	172	87.8	39	PCT-US01-11954-13	Sequence 13, Appli
26	172	87.8	39	PCT-US01-11954-11	Sequence 11, Appli
27	172	87.8	29	US-10-399-602-13	Sequence 13, Appli
28	172	87.8	29	US-10-399-602-32	Sequence 32, Appli
29	172	87.8	39	US-10-399-602-13	Sequence 13, Appli
30	172	87.8	36	US-10-014-162-40	Sequence 40, Appli
31	172	87.8	33	US-10-014-162-4	Sequence 4, Appli
32	172	87.8	26	US-10-014-162-60	Sequence 6, Appli
33	172	87.8	26	US-10-014-162-64	Sequence 64, Appli
34	172	87.8	33	PCT-US02-01183-32	Sequence 32, Appli
35	172	87.8	39	US-10-466-493A-32	Sequence 32, Appli
36	172	87.8	33	US-10-712-124-72	Sequence 72, Appli

Run on: December 29, 2004, 15:11:45 ; Search time 25 seconds
           (without alignments)
           72.768 Million cell updates/sec

Title:
Perfect score: 196
Sequence: 1 SIALADDAPFRERARLLAALERHHWINSYMHKLLVLDAP 39

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 187395 seqs, 46645940 residues

Total number of hits satisfying chosen parameters: 187395

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Databases :   Pending_Patents_AA_Nov:*
                 1: /rgm2_6/prcdata/2/paa/PCT_NEW_COMB.pep:*
                 2: /rgm2_6/prcdata/2/paa/US06_NEW_COMB.pep:*
                 3: /rgm2_6/prcdata/2/paa/US07_NEW_COMB.pep:*
                 4: /rgm2_6/prcdata/2/paa/US08_NEW_COMB.pep:*
                 5: /rgm2_6/prcdata/2/paa/US09_NEW_COMB.pep:*
                 6: /rgm2_6/prcdata/2/paa/US10_NEW_COMB.pep:*
                 7: /rgm2_6/prcdata/2/paa/US11_NEW_COMB.pep:*
                 8: /rgm2_6/prcdata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	196	100.0	39	5	US-09-999-608-160	Sequence 160, App
2	196	100.0	39	1	US-09-999-608-168	Sequence 168, App
3	55.5	28.3	528	6	US-10-990-328-12930	Sequence 12930, A
4	55.5	28.3	528	6	US-10-990-328-12929	Sequence 12929, A
5	55.5	28.3	528	6	US-10-990-328-12931	Sequence 12931, A
6	55.5	28.3	528	6	US-09-990-328-12934	Sequence 12934, A
7	28.3		10		US-10-732-923-4371	Sequence 4371, Ap
8	28.3		308	1	PCT-US04-12017-56061	Sequence 56061, A
9	50	25.5	308	1	PCT-US02-09107B-75211	Sequence 75211, A
10	49.5	25.3	428	1	PCT-US02-09107B-72040	Sequence 72040, A
11	49.5	25.3	558	1	PCT-US02-09107B-63818	Sequence 63818, A

39	171	87.2	34	5	US-10-014-162-42	Sequence 42, Appl
40	170	86.7	33	23	PCT-US02-09107B-23	Sequence 37, Appl
41	170	86.7	33	5	PCT-US04-13723-27	Sequence 27, A
42	170	86.7	33	26	US-10-014-162-1	Sequence 23, Appl
43	170	86.7	33	30	US-10-428-377-23	Sequence 23, Appl
44	170	86.7	33	30	US-10-428-377-27	Sequence 27, Appl
45	167	85.2	33	26	US-10-014-162-43	Sequence 43, Appl

Run on: December 29, 2004, 15:23:17 ; Search time 39 seconds
           (without alignments)
           96.217 Million cell updates/sec

Title:
Perfect score: 196
Sequence: 1 SIALADDAPFRERARLLAALERHHWINSYMHKLLVLDAP 39

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Databases :   PIR_79:**
                 1: pir1:*
                 2: pir2:*

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	196	100.0	669	1	PCT-US02-09107B-67679	Sequence 67679, A
2	196		338	1	PCT-US02-09107B-67439	Sequence 67439, A
3	55.5	28.3	330	1	US-60-612-215-23	Sequence 23, Appl
4	55.5	28.3	4442	1	US-10-488-197-69	Sequence 69, Appl
5	47.5	24.5	239	1	US-10-732-923-53679	Sequence 53679, A
6	47.5	24.5	389	1	PCT-US02-09107B-53679	Sequence 6, Appl
7	47	24.0	389	1	US-10-408-765-1757	Sequence 1757, A
8	47	24.0	389	1	PCT-US04-37204-6461	Sequence 6461, A
22	48	24.5	1272	1	PCT-US02-09107B-44356	Sequence 44356, A
23	48	24.5	161	1	PCT-US02-09107B-78249	Sequence 78249, A
24	47.5	24.5	199	1	US-10-732-923-12932	Sequence 12932, A
44	46	23.5	525	1	US-10-990-328-12932	Sequence 12932, A
45	46	23.5	593	1	US-10-990-328-12933	Sequence 12933, A
46	46	23.5	549	1	PCT-US02-09107B-62828	Sequence 62828, A

Report 1 (right block)

Title: US-10-014-162-1
Perfect score: 196
Sequences: 1 SLALADDAFREERARLLAALEERRWLWSYWHKKLLVLDAR 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 segs, 575374646 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : 1: UniProt_021*
1: uniprot_sprot;*
2: uniprot_trembl;*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Pred. No.	Query Match	Length	DB	ID	Description
1	100.0		100	100	2	Q96A98	Q96A98 homo sapien
2	87.8		119	159	2	Q91W27	Q91W27 mus muscu
3	67.3		59	90	2	Q91ZA0	Q91ZA0 mus muscu
4	62.5		85	135	2	Q96GJ4	Q96GJ4 homo sapien
5	57.7			603	2	Q9EYV2	Q9EYV2 rhizobium l
6	35.7			607	2	Q98AV5	Q98AV5 rhizobium l
7	35.2			69	2	Q6G5J4	Q6G5J4 Bdellovibrio
8	35.0				2	Q8GBX4	Q8GBX4 polyangium
9	34.4			356	2	Q6G9V5	Q6G9V5 euca lyptus
10	34.4			493	2	Q6NIN1	Q6NIN1 rhodopseudo
11	34.4			493	2	Q6NIN1	Q6NIN1 rhodopseudo
12	34.0			817	2	Q8RN61	Q8RN61 chromobacte
13	30.4				2	Q8FIS5	Q8FIS5 escherichia
14	30.4			4555	2	P36679	P36679 escherichia
15	30.1			1063	2	Q7N261	Q7N261 chromobacte
16	30.1			206	2	COAE_ECOL6	COAE_ECOL6
17	29.8			206	2	COAE_ECOLI	COAE_ECOLI
18	29.8			382	2	Q82JU8	Q82JU8 streptomyce
19	29.8			380	2	Q82II8	Q82II8 streptomyce
20	29.6			467	2	Q6M2V8	Q6M2V8 homo sapien
21	29.6			467	2	Q8NIH5	Q8NIH5 homo sapien
22	29.6				2	Q8STN5	Q8STN5 encephalito
23	29.6				2	Q8NLH5	Q8NLH5 homo sapien
24	29.6				2	CAE4519	CAE4519
25	29.6				2	Q6Q909	Q6Q909
26	29.6			590	2	Q6SKX1	Q6SKX1 homo sapien
27	29.6			590	2	Q6SKX1	Q6SKX1 homo sapien
28	57.5				2	Q8N865	Q8N865 homo sapien
29	57.5			611	2	AAH60879	AAH60879 homo sapien
30	57.3			206	2	Q8HXQ5	Q8HXQ5
31	57				2	COAE_SHIFL	COAE_SHIFL
32	57			362	2	Q7M136	Q7M136 gloeobacter
33	57				2	COAE_PSEAE	COAE_PSEAE
34	56.5			524	2	Q9HVP8	Q9HVP8 pseudomonas
35	56.5				2	P5G256	P5G256 klebsiella

Report 2 (left block)

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

3: pir3;*
4: pir4;*

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	58.5	29.8	206	2	C85693	probable DNA repai
2	58.5	29.8	206	2	C90642	probable DNA repai
3	58.5	29.8	611	2	G61732	yicE protein - Esc
4	57	29.1	203	2	G83177	probable sodium/hy
5	57	29.1	524	2	E83078	conserved hypothet
6	56.5	28.8	206	2	RXKBAP	RXKBAP
7	56.5	28.8	206	2	ACO520	conserved hypothet
8	55	28.1	484	2	F72450	nif-specific regul
9	55	28.1	518	2	C96018	probable starch sy
10	53.5	27.3	366	2	S60176	regulatory protein
11	53	27.0	1078	2	T42666	hypothetical prote
12	53	27.0	168	2	T19745	hypothetical prote
13	52.5	26.5	572	2	G81712	nitrate centromere
14	52	26.5	605	2	H82791	hypothetical prote
15	52	26.5	213	2	C82078	conserved hypothet
16	52	26.5	519	2	C25878	nif-specific regul
17	51.5	26.3	1112	2	T30202	probable chitin sy
18	51.5	26.3	525	2	A02282	hypothetical prote
19	51.5	26.3	204	2	A10285	hypothetical prote
20	51	26.0	309	2	T08021	com,impetent
21	51	26.0	414	2	AE3325	penicillin-binding
22	51	26.0	572	2	S75823	hypothetical prote
23	51	26.0	605	2	T34345	hypothetical prote
24	51	26.0	330	2	S01066	regulatory protein
25	50.5	25.8	522	2	H87625	nid-1,4-beta-xyla
26	50.5	25.8	546	2	S01927	ABC-specific regul
27	50.5	25.8	616	2	S02340	nid-specific regul
28	50.5	25.8	1852	2	JCS546	chitin synthase (B
29	50.5	25.8	512	2	F82482	hypothetical prote
30	50.5	25.8	174	2	JE0305	propanediol dehydr
31	50	25.5	306	2	D70657	hypothetical prote
32	50	25.5	306	2	S45204	probable ABC-t
33	50	25.5	308	2	S45304	probable ABC-type
34	50	25.5	308	2	C85496	hypothetical prote
35	50	25.5	308	2	C90645	hypothetical prote
36	50	25.5	309	2	F75516	ABC transporter (A
37	50	25.5	311	2	AB1516	ABC transporter (A
38	50	25.5	326	2	S54042	hypothetical prote
39	50	25.5	512	2	D93025	hypothetical prote
40	50	25.5	715	2	B83322	regulatory protein
41	50	25.5	1086	2	JC6079	chitin synthase (B
42	50	25.5	1195	2	S61886	chitin synthase (E
43	50	25.5	1498	2	S78102	chitin synthase (E

36	56	28.6	588	2	Q9D5Y0	Q9d5y0 m_mus muscu
37	55.5	28.3	290	2	Q89TF0	Q89tf0 bradyrhizob
38	55.5	28.3	295	2	Q9AMW7	Q9amw7 bradyrhizob
39	55.5	28.3	433	2	Q8F4L8	Q8f4l8 xanthomonas
40	55.5	28.3	521	2	Q93T73	Q93t73 pseudomonas
41	55.5	28.3	736	2	Q8BL19	Q8bl19 mus musculu
42	55.5	28.3	737	2	Q8N3E9	Q8n3e9 homo sapien
43	55.5	28.3	757	2	Q8TF37	Q8tf37 homo sapien
44	55.5	28.3	785	2	Q8X2J0	Q8x2j0 mus musculi
45	55.5	28.3	789	2	Q8TEC1	Q8tec1 homo sapien